SEQUENCE LISTING

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<120>   HUMAN POLYPEPTIDES CAUSING OR LEADING TO THE KILLING
        OF CELLS   INCLUDING LYMPHOID TUMOR CELLS

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<140>   10/001934
<141>   2001-11-15

<150>   PCT/US01/15625
<151>   2001-05-14

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<170>   PatentIn version 3.0

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aaaaccgtct atcagggcga tggcccacta cgagaaccat caccctaatc aagttttttg    2280

gggtcgaggt gccgtaaagc actaaatcgg aaccctaaag ggagcccccg atttagagct    2340

tgacggggaa agccggcgaa cgtggcgaga aaggaaggga agaaagcgaa aggagcgggc    2400

gctagggcgc tggcaagtgt agcggtcacg ctgcgcgtaa ccaccacacc cgccgcgctt    2460

aatgcgccgc tacagggcgc gtgctagcca tgtgagcaaa aggccagcaa aaggccagga    2520

accgtaaaaa ggccgcgttg ctggcgtttt ccataggct ccgcccccct gacgagcatc    2580

acaaaaatcg acgctcaagt cagaggtggc gaaacccgac aggactataa agataccagg    2640

cgtttccccc tggaagctcc ctcgtgcgct ctcctgttcc gaccctgccg cttaccggat    2700

acctgtccgc ctttctccct tcgggaagcg tggcgctttc tcatagctca cgctgtaggt    2760

atctcagttc ggtgtaggtc gttcgctcca agctgggctg tgtgcacgaa cccccccgttc   2820

agtccgaccg ctgcgcctta tccggtaact atcgtcttga gtccaacccg gtaagacacg    2880

acttatcgcc actggcagca gccactggta acaggattag cagagcgagg tatgtaggcg    2940

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gaaaaaaagg atctcaagaa gatcctttga tcttttctac ggggtctgac gctcagtgga    3180

acgaaaactc acgttaaggg attttggtca gatctagcac caggcgttta agggcaccaa    3240

taactgcctt aaaaaaatta cgccccgccc tgccactcat cgcagtactg ttgtaattca    3300

ttaagcattc tgccgacatg gaagccatca caaacggcat gatgaacctg aatcgccagc    3360

ggcatcagca ccttgtcgcc ttgcgtataa tatttgccca tagtgaaaac ggggggcgaag   3420

aagttgtcca tattggctac gtttaaatca aaactggtga aactcaccca gggattggct    3480

gagacgaaaa acatattctc aataaaccct ttagggaaat aggccaggtt ttcaccgtaa    3540

cacgccacat cttgcgaata tatgtgtaga aactgccgga aatcgtcgtg gtattcactc    3600
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cagagcgatg aaaacgtttc agtttgctca tggaaaacgg tgtaacaagg gtgaacacta   3660

tcccatatca ccagctcacc gtctttcatt gccatacgga actccgggtg agcattcatc   3720

aggcgggcaa gaatgtgaat aaaggccgga taaaacttgt gcttattttt ctttacggtc   3780

tttaaaaagg ccgtaatatc cagctgaacg gtctggttat aggtacattg agcaactgac   3840

tgaaatgcct caaaatgttc tttacgatgc cattgggata tatcaacggt ggtatatcca   3900

gtgatttttt tctccatttt agcttcctta gctcctgaaa atctcgataa ctcaaaaaat   3960

acgcccggta gtgatcttat ttcattatgg tgaaagttgg aacctcaccc gacgtctaat   4020

gtgagttagc tcactcatta ggcaccccag gctttacact ttatgcttcc ggctcgtatg   4080

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gaatt                                                                4145
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<210> 73
<211> 120
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC1-VH
<222> (1)..(120)

<400> 73

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Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1               5                   10                  15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20                  25                  30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
    50                  55                  60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Gln Tyr Gly His Arg Gly Gly Phe Asp His Trp Gly Gln
                100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
            115                 120
```

<210> 74
<211> 109
<212> PRT
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<213> artificial sequence

<220>
<221> MS-GPC1-VL
<222> (1)..(109)

<400> 74

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
                20                  25                  30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35                  40                  45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Asn Glu
                85                  90                  95

Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
                100                 105


<210> 75
<211> 118
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC6-VH
<222> (1)..(118)

<400> 75

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
                20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
            35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
        50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Tyr Gly Arg Tyr Ser Pro Asp Leu Trp Gly Gln Gly Thr

Leu Val Thr Val Ser Ser
        115

<210>  76
<211>  110
<212>  PRT
<213>  artificial sequence

<220>
<221>  MS-GPC6-VL
<222>  (1)..(110)

<400>  76

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5               10              15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20              25              30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35              40              45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
        50              55              60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65              70              75              80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Ser Asn Leu Pro
            85              90              95

Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            100             105             110

<210>  77
<211>  120
<212>  PRT
<213>  artificial sequence

<220>
<221>  MS-GPC8-VH
<222>  (1)..(120)

<400>  77

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1               5               10              15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20              25              30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35              40              45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
    50              55              60

```
Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65              70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
            100                 105             110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>    78
<211>    109
<212>    PRT
<213>    artificial sequence

<220>
<221>    MS-GPC8-VL
<222>    (1)..(109)

<400>    78

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5               10                  15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
                20                  25                  30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35                  40                  45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65              70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Pro Gln
                85                  90                  95

Ala Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105


<210>    79
<211>    120
<212>    PRT
<213>    artificial sequence

<220>
<221>    MS-GPC10-VH
<222>    (1)..(120)

<400>    79

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1               5               10                  15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
```

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
    50   55   60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85   90   95

Cys Ala Arg Gln Leu His Tyr Arg Gly Gly Phe Asp Leu Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
            115   120

<210>   80
<211>   109
<212>   PRT
<213>   artificial sequence

<220>
<221>   MS-GPC10-VL
<222>   (1)..(109)

<400>   80

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Thr Met
                85   90   95

Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100   105

<210>   81
<211>   120
<212>   PRT
<213>   artificial sequence

<220>
<221> MS-GPC8-6-VH
<222> (1)..(120)

<400> 81
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1   5   10   15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20   25   30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
    50   55   60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85   90   95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 82
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-6-VL
<222> (1)..(109)

<400> 82

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Asp His
                85   90   95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100   105

<210>   83
<211>   120
<212>   PRT
<213>   artificial sequence

<220>
<221>   MS-GPC8-10-VH
<222>   (1)..(121)

<400>   83

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1   5   10   15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20   25   30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
            35   40   45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
    50   55   60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85   90   95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
            115   120

<210>   84
<211>   109
<212>   PRT
<213>   artificial sequence

<220>
<221>   MS-GPC8-10-VL
<222>   (1)..(109)

<400>   84

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
            35   40   45

```
Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50              55              60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65              70              75              80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Ile Arg
                85              90              95
His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100             105
```

<210> 85
<211> 120
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-17-VH
<222> (1)..(120)

<400> 85
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Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1               5               10              15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20              25              30
Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
            35              40              45
Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
    50              55              60
Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65              70              75              80
Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85              90              95
Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
            100             105             110
Gly Thr Leu Val Thr Val Ser Ser
            115             120
```

<210> 86
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-17-VL
<222> (1)..(109)

<400> 86

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
        50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Ser Val
                85   90   95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
                100   105

<210>   87
<211>   120
<212>   PRT
<213>   artificial sequence

<220>
<221>   MS-GPC8-27-VH
<222>   (1)..(120)

<400>   87
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1   5   10   15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20   25   30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
        50   55   60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85   90   95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
                100   105   110

Gly Thr Leu Val Thr Val Ser Ser
            115   120

<210>   88

<211> 115
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-27-VL
<222> (1)..(115)

<400> 88
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20   25   30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65   70   75   80

Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Asn
                85   90   95

Val His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100   110   115

<210> 89
<211> 120
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-6-13-VH
<222> (1)..(120)

<400> 89
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1   5   10   15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20   25   30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
    50   55   60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85   90   95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln

Gly Thr Leu Val Thr Val Ser Ser
          115   120

<210> 90
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-6-13-VL
<222> (1)..(109)

<400> 90
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Ala Asn
              20   25   30

Tyr Val Thr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
          35   40   45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
      50   55   60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65   70   75   80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Asp His
                  85   90   95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
              100   105

<210> 91
<211> 120
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-10-57-VH
<222> (1)..(120)

<400> 91
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1   5   10   15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
              20   25   30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
          35   40   45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
      50   55   60

```
Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65              70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115             120


<210>   92
<211>   109
<212>   PRT
<213>   artificial sequence

<220>
<221>   MS-GPC8-10-57-VL
<222>   (1)..(109)

<400>   92
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Asn Asn
            20                  25                  30

Tyr Val Gln Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65              70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Ile Arg
                85                  90                  95

His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105


<210>   93
<211>   120
<212>   PRT
<213>   artificial sequence

<220>
<221>   MS-GPC8-27-41-VH
<222>   (1)..(120)

<400>   93
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1               5                   10                  15
```

```
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20                  25                  30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
    50                  55                  60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
            115                 120
```

```
<210>   94
<211>   109
<212>   PRT
<213>   artificial sequence

<220>
<221>   MS-GPC8-27-41-VL
<222>   (1)..(108)

<400>   94
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1               5                   10                  15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Asn Asn
            20                  25                  30

Tyr Val Gln Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Asn Val
                85                  90                  95

His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105
```

1